

# SEQUENCE LISTING

<110> Walke, D. Wade  
 Friddle, Carl Johan  
 Mathur, Brian  
 Turner, C. Alexander Jr.

<120> Novel Human GABA Receptors and  
 Polynucleotides Encoding the Same

<130> LEX-0195-USA

<150> US 60/214,083

<151> 2000-06-27

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1398

<212> DNA

<213> homo sapiens

<400> 1

atgggtcctt	tgaagctgtt	tctcttctcc	ccttttcttc	tcgggagtc	aagtagagg	60
gtgggttg	tcttctgtt	actgacctg	catttggaa	actgtgttg	taaggcagat	120
gatgaagatg	atgaggtatt	aacggggaac	aaaacctggg	tcttggcccc	aaaaattcat	180
gaaggagata	tcacacaaat	tctgaattca	ttgcttcaag	gctatgacaa	taaaacttcgt	240
ccagatatag	gagtgaggcc	cacrgtaatt	gaaactgatg	tttatgtaaa	cagcatttga	300
ccagttgatc	caattaatat	ggaatatata	atagatatata	tttttgccta	aacctggttt	360
gacagtcgtt	taaaatccaa	tagtaccatg	aaagtgccta	tgcttaacag	taatatgggt	420
ggaaaaattt	ggattctctg	cactttcttc	agaaactcaa	gaaaatctga	tgctcactgg	480
ataacaactc	ctaactcgtc	gcttcgaatt	tggaatgatg	gacgagttct	gtatactcta	540
agattgcaca	ttaatgcaga	atgttatctt	cagcttcata	actttcccat	ggatgaacat	600
tcctgtccac	tggaattttc	aagctatgga	taccctaaaa	atgaaattga	gtataagttg	660
aaaaagccct	ccgtagaagt	ggctgatcct	aaatactgga	gattatatca	gtttgcattt	720
gtagggttac	ggaactcaac	tgaatacact	cacacgatct	cwggggatta	kggttatcatg	780
acaatttttt	ttgacctgag	cagaagaatg	ggatatattca	ctattcagac	ctacattcca	840
tgcatctctg	cagttgttct	ttcttgggtg	tctttttgga	tcaataaaga	tgcatgtgctc	900
cgcaagaacat	cgttgggtat	cactacagtt	ctgactatga	caaccttgag	tacaattgcc	960
aggaagtcct	tacctaaggt	ttcttatgtg	actgcgatgg	atctctttgt	ttctgtttgt	1020
ttcatttttg	tttttgcagc	cttgatggaa	tatggaacct	tgcatatttt	taccagcaac	1080
caaaaaggaa	agactgctac	taaaagcaga	aagctaaaaa	ataaagcctc	gatgactcct	1140
ggcttccatc	ctggatccac	tctgattcca	atgaataata	tttctgtgcc	cgcaagaagat	1200
gattatgggt	atcagtggtt	ggagggcaca	gattgtgcga	gcttcttctg	ttgctttgaa	1260
gactgcagaa	caggatcttg	gaggggaagg	aggatacaca	tacgcattgc	caaaattgac	1320
tcttatctta	gaatattttt	cccaaccgct	tttgcctgtg	tcaacttggt	ttattggggt	1380
ggctatcttt	actttataa					1398

<210> 2

<211> 465

<212> PRT

<213> homo sapiens

<400> 2

Met Gly Pro Leu Lys Ala Phe Leu Phe Ser Pro Phe Leu Leu Arg Ser  
 1 5 10 15  
 Gln Ser Arg Gly Val Arg Leu Val Phe Leu Leu Leu Thr Leu His Leu  
 20 25 30  
 Gly Asn Cys Val Asp Lys Ala Asp Asp Glu Asp Asp Glu Asp Leu Thr  
 35 40 45  
 Val Asn Lys Thr Trp Val Leu Ala Pro Lys Ile His Glu Gly Asp Ile  
 50 55 60  
 Thr Gln Ile Leu Asn Ser Leu Leu Gln Gly Tyr Asp Asn Lys Leu Arg  
 65 70 75 80  
 Pro Asp Ile Gly Val Arg Pro Thr Val Ile Glu Thr Asp Val Tyr Val  
 85 90 95  
 Asn Ser Ile Gly Pro Val Asp Pro Ile Asn Met Glu Tyr Thr Ile Asp  
 100 105 110  
 Ile Ile Phe Ala Gln Thr Trp Phe Asp Ser Arg Leu Lys Phe Asn Ser  
 115 120 125  
 Thr Met Lys Val Leu Met Leu Asn Ser Asn Met Val Gly Lys Ile Trp  
 130 135 140  
 Ile Pro Asp Thr Phe Phe Arg Asn Ser Arg Lys Ser Asp Ala His Trp  
 145 150 155 160  
 Ile Thr Thr Pro Asn Arg Leu Leu Arg Ile Trp Asn Asp Gly Arg Val  
 165 170 175  
 Leu Tyr Thr Leu Arg Leu Thr Ile Asn Ala Glu Cys Tyr Leu Gln Leu  
 180 185 190  
 His Asn Phe Pro Met Asp Glu His Ser Cys Pro Leu Glu Phe Ser Ser  
 195 200 205  
 Tyr Gly Tyr Pro Lys Asn Glu Ile Glu Tyr Lys Trp Lys Lys Pro Ser  
 210 215 220  
 Val Glu Val Ala Asp Pro Lys Tyr Trp Arg Leu Tyr Gln Phe Ala Phe  
 225 230 235 240  
 Val Gly Leu Arg Asn Ser Thr Glu Ile Thr His Thr Ile Ser Gly Asp  
 245 250 255  
 Tyr Val Ile Met Thr Ile Phe Phe Asp Leu Ser Arg Arg Met Gly Tyr  
 260 265 270  
 Phe Thr Ile Gln Thr Tyr Ile Pro Cys Ile Leu Thr Val Val Leu Ser  
 275 280 285  
 Trp Val Ser Phe Trp Ile Asn Lys Asp Ala Val Pro Ala Arg Thr Ser  
 290 295 300  
 Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Leu Ser Thr Ile Ala  
 305 310 315 320  
 Arg Lys Ser Leu Pro Lys Val Ser Tyr Val Thr Ala Met Asp Leu Phe  
 325 330 335  
 Val Ser Val Cys Phe Ile Phe Val Phe Ala Ala Leu Met Glu Tyr Gly  
 340 345 350  
 Thr Leu His Tyr Phe Thr Ser Asn Gln Lys Gly Lys Thr Ala Thr Lys  
 355 360 365  
 Asp Arg Lys Leu Lys Asn Lys Ala Ser Met Thr Pro Gly Leu His Pro  
 370 375 380  
 Gly Ser Thr Leu Ile Pro Met Asn Asn Ile Ser Val Pro Gln Glu Asp  
 385 390 395 400  
 Asp Tyr Gly Tyr Gln Cys Leu Glu Gly Lys Asp Cys Ala Ser Phe Phe  
 405 410 415  
 Cys Cys Phe Glu Asp Cys Arg Thr Gly Ser Trp Arg Glu Gly Arg Ile  
 420 425 430  
 His Ile Arg Ile Ala Lys Ile Asp Ser Tyr Ser Arg Ile Phe Phe Pro

435 440 445  
Thr Ala Phe Ala Leu Phe Asn Leu Val Tyr Trp Val Gly Tyr Leu Tyr  
450 455 460  
Leu  
465

<210> 3  
<211> 771  
<212> DNA  
<213> homo sapiens

<400> 3  
atgggtcctt tgaagcttt tctcttctcc ccttttcttc tgcggagtca aagtagaggg 60  
gtgaggttgg tcttcttgg actgacctg catttgggaa actgtgttga taaggcagat 120  
gatgaagatg atgaggattt aacggtgaac aaaacctggg tcttggcccc aaaaattcat 180  
gaaggagata tcacacaaat tctgaattca ttgcttcaag gctatgacaa taaacttcgt 240  
ccagatatag gagtgaggcc cacagtaatt gaaactgatg tttatgtaaa cagcatttga 300  
ccagttgatc caattaatat ggaatataca atagatataa tttttgcccc aacctgggtt 360  
gcagtcggtt taaaattcaa tagtaccatg aaagtgttta tgcttaacag taatatgtgt 420  
ggaaaaattt ggattcctga cactttcttc agaaactcaa gaaaacttga tgctcactgg 480  
atacaaacct ctaatcgtct gcttcgaatt tggaaatgatg gacgagttct gtatactcta 540  
agattgacaa ttaatgcaga atgttatctt cagcttcata actttcccat ggatgaacat 600  
tctctgtcac tggaaatttc aagctatgga taccctaaaa atgaaattga gataaagttg 660  
aaaagccct ccgtagaagt ggctgatcct aaatactgga gattatatca gtttgcattt 720  
gtaggggttac ggaactcaac tgaatacact cacacgatct ctgggggatta g 771

<210> 4  
<211> 256  
<212> PRT  
<213> homo sapiens

<400> 4  
Met Gly Pro Leu Lys Ala Phe Leu Phe Ser Pro Phe Leu Leu Arg Ser  
1 5 10 15  
Gln Ser Arg Gly Val Arg Leu Val Phe Leu Leu Thr Leu His Leu  
20 25 30  
Gly Asn Cys Val Asp Lys Ala Asp Asp Glu Asp Asp Glu Asp Leu Thr  
35 40 45  
Val Asn Lys Thr Trp Val Leu Ala Pro Lys Ile His Glu Gly Asp Ile  
50 55 60  
Thr Gln Ile Leu Asn Ser Leu Leu Gln Gly Tyr Asp Asn Lys Leu Arg  
65 70 75 80  
Pro Asp Ile Gly Val Arg Pro Thr Val Ile Glu Thr Asp Val Tyr Val  
85 90 95  
Asn Ser Ile Gly Pro Val Asp Pro Ile Asn Met Glu Tyr Thr Ile Asp  
100 105 110  
Ile Ile Phe Ala Gln Thr Trp Phe Asp Ser Arg Leu Lys Phe Asn Ser  
115 120 125  
Thr Met Lys Val Leu Met Leu Asn Ser Asn Met Val Gly Lys Ile Trp  
130 135 140  
Ile Pro Asp Thr Phe Phe Arg Asn Ser Arg Lys Ser Asp Ala His Trp  
145 150 155 160  
Ile Thr Thr Pro Asn Arg Leu Leu Arg Ile Trp Asn Asp Gly Arg Val  
165 170 175  
Leu Tyr Thr Leu Arg Leu Thr Ile Asn Ala Glu Cys Tyr Leu Gln Leu  
180 185 190

His Asn Phe Pro Met Asp Glu His Ser Cys Pro Leu Glu Phe Ser Ser  
 195 200 205  
 Tyr Gly Tyr Pro Lys Asn Glu Ile Glu Tyr Lys Trp Lys Lys Pro Ser  
 210 215 220  
 Val Glu Val Ala Asp Pro Lys Tyr Trp Arg Leu Tyr Gln Phe Ala Phe  
 225 230 235 240  
 Val Gly Leu Arg Asn Ser Thr Glu Ile Thr His Thr Ile Ser Gly Asp  
 245 250 255

<210> 5  
 <211> 1568  
 <212> DNA  
 <213> homo sapiens

<400> 5  
 ggtgcactgc ctttccacac tctcccttct gtactcagcc agctgctgct gaggtgggag 60  
 gaaaagtctt ggctgggaga attgagctag tgcagcacac gtaaaaaagc gattccgatg 120  
 ggctccttga aagcttttct ctctccctct tttctctcgc ggagtcacaa tagaggggtg 180  
 aggttgggtct tcttgttact gacctgtcat ttgggaaact gtgtgtgataa ggcagatgat 240  
 gaagatgatg aggatttaac ggtgaacaaa acctgggtct tggcccaaaa aattcatgaa 300  
 ggagatcatca cacaaattct gaattcattg ctccaaggct atgacaataa acttcgtcca 360  
 gatataaggag tgagggccac rgtaattgaa actgatgttt atgtaaacag cattggacca 420  
 gttgatccaa ttaatatgga atatacaata gatataattt ttgcccacac ctggtttgac 480  
 agtcgtttaa aattcaatag taccatgaaa gtgcttatgc ttaacagtaa tatggttgga 540  
 aaaatttggg ttctcgacac ttctctcaga aactcaagaa aatctgatgc tcactggata 600  
 acaactccta atcgtctgct tcgaatttgg aatgatggac gagttctgta tactctaaga 660  
 ttgacaatta atgcagaatg ttatctctcag ctccataact ttcccatgga tgaacattcc 720  
 tgtccactgg aattttcaag ctatggatac cctaaaaatg aaatttgagta taagtgga 780  
 aagccctcgc tagaagtggc tgatctctaa tactggagat tataatcagtt tgcatttgta 840  
 gggttacgga actcaactga aatcactcac acgatctcwg gggattakgt tatcatgaca 900  
 attttttttg acctgagcag aagaatggga tatttctacta ttcagaecta cattccatgc 960  
 attctgacag ttgttcttctc ttgggtgtct ttttggatca ataaagatgc agtgcctgca 1020  
 agaacatcgt tgggtatcac tacagttctg actatgacaa ccctgagtac aattgccagg 1080  
 aagtcctttac ctaaggtttc ttatgtgact gcgatggatc tctttgtttc tgtttgttcc 1140  
 attttttgtt ttgcagcctt gatggaaatg ggaaccttgc attattttac cagcaaccaa 1200  
 aaaggaaaga ctgtactata agacagaaaag ctaaaaaata aagcctcgat gactcctggt 1260  
 ctccatctcg gatccactct gattccaatg aataatatatt ctgtgccgca agaagatgat 1320  
 tatgggtatc agtgtttgga gggcaaaagt tgtgccagct tctttctgtt ctttgaagac 1380  
 tgcagaacag gatcttggag ggaaggaaag atacacatac gcattgccaa aattgactct 1440  
 tattctagaa tatttttccc aaccgctttt gccctgttca acttgggttta ttgggttggc 1500  
 tatctttact tataaaatct acttcataag caaaaaatca aagaagctct gacttaaat 1560  
 tcaagtag 1568